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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/840,787

DATE: 06/15/2001

TIME: 14:40:49

Input Set : N:\Crf3\RULE60\09840787.txt

Output Set: N:\CRF3\06152001\I840787.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

## 5 (i) APPLICANT: Lal, Preeti

6 Hillman, Jennifer L.

7 Bandman, Olga

8 Shah, Purvi

9 Au-Young, Janice

10 Yue, Henry

11 Guegler, Karl J.

12 Corley, Neil C.

## 14 (ii) TITLE OF INVENTION: HUMAN REGULATORY MOLECULES

## 16 (iii) NUMBER OF SEQUENCES: 98

## 18 (iv) CORRESPONDENCE ADDRESS:

19 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

20 (B) STREET: 3174 Porter Drive

21 (C) CITY: Palo Alto

22 (D) STATE: CA

23 (E) COUNTRY: USA

24 (F) ZIP: 94304

## 26 (v) COMPUTER READABLE FORM:

27 (A) MEDIUM TYPE: Diskette

28 (B) COMPUTER: IBM Compatible

29 (C) OPERATING SYSTEM: DOS

30 (D) SOFTWARE: FastSEQ for Windows Version 2.0

## 32 (vi) CURRENT APPLICATION DATA:

C--&gt; 33 (A) APPLICATION NUMBER: US/09/840,787

C--&gt; 34 (B) FILING DATE: 23-Apr-2001

35 (C) CLASSIFICATION:

## 37 (vii) PRIOR APPLICATION DATA:

38 (A) APPLICATION NUMBER: 09/518,865

39 (B) FILING DATE:

## 41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: Billings, Lucy J.

43 (B) REGISTRATION NUMBER: 36,749

44 (C) REFERENCE/DOCKET NUMBER: PF-0356 US

## 46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: 415-855-0555

48 (B) TELEFAX: 415-845-4166

49 (C) TELEX:

## 52 (2) INFORMATION FOR SEQ ID NO: 1:

## 54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 151 amino acids

56 (B) TYPE: amino acid

57 (C) STRANDEDNESS: single

58 (D) TOPOLOGY: linear

## 60 (vii) IMMEDIATE SOURCE:

61 (A) LIBRARY: U937NOT01

ENTERED

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62 (B) CLONE: 133

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

66	Met	Thr	Asn	Glu	Glu	Pro	Leu	Pro	Lys	Lys	Val	Arg	Leu	Ser	Glu	
67				5						10					15	
68	Thr	Asp	Phe	Lys	Val	Met	Ala	Arg	Asp	Glu	Leu	Ile	Leu	Arg	Trp	
69				20						25					30	
70	Lys	Gln	Tyr	Glu	Ala	Tyr	Val	Gln	Ala	Leu	Glu	Gly	Lys	Tyr	Thr	
71				35						40					45	
72	Asp	Leu	Asn	Ser	Asn	Asp	Val	Thr	Gly	Leu	Arg	Glu	Ser	Glu	Glu	
73				50						55					60	
74	Lys	Leu	Lys	Gln	Gln	Gln	Gln	Glu	Ser	Ala	Arg	Arg	Glu	Asn	Ile	
75				65						70					75	
76	Leu	Val	Met	Arg	Leu	Ala	Thr	Lys	Glu	Gln	Glu	Met	Gln	Glu	Cys	
77				80						85					90	
78	Thr	Thr	Gln	Ile	Gln	Tyr	Leu	Lys	Gln	Val	Gln	Gln	Pro	Ser	Val	
79				95						100					105	
80	Ala	Gln	Leu	Arg	Ser	Thr	Met	Val	Asp	Pro	Ala	Ile	Asn	Leu	Phe	
81				110						115					120	
82	Phe	Leu	Lys	Met	Lys	Gly	Glu	Leu	Glu	Gln	Thr	Lys	Asp	Lys	Leu	
83				125						130					135	
84	Glu	Gln	Ala	Gln	Asn	Glu	Leu	Ser	Ala	Trp	Lys	Phe	Thr	Pro	Asp	
85				140						145					150	

86 Arg

89 (2) INFORMATION FOR SEQ ID NO: 2:

91 (i) SEQUENCE CHARACTERISTICS:

92 (A) LENGTH: 185 amino acids

93 (B) TYPE: amino acid

94 (C) STRANDEDNESS: single

95 (D) TOPOLOGY: linear

97 (vii) IMMEDIATE SOURCE:

98 (A) LIBRARY: U937NOT01

99 (B) CLONE: 1762

101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

103	Met	Leu	Thr	Leu	Ala	Ser	Lys	Leu	Lys	Arg	Asp	Asp	Gly	Leu	Lys	
104				5						10					15	
105	Gly	Ser	Arg	Thr	Ala	Ala	Thr	Ala	Ser	Asp	Ser	Thr	Arg	Arg	Val	
106				20						25					30	
107	Ser	Val	Arg	Asp	Lys	Leu	Leu	Val	Lys	Glu	Val	Ala	Glu	Leu	Glu	
108				35						40					45	
109	Ala	Asn	Leu	Pro	Cys	Thr	Cys	Lys	Val	His	Phe	Pro	Asp	Pro	Asn	
110				50						55					60	
111	Lys	Leu	His	Cys	Phe	Gln	Leu	Thr	Val	Thr	Pro	Asp	Glu	Gly	Tyr	
112				65						70					75	
113	Tyr	Gln	Gly	Gly	Lys	Phe	Gln	Phe	Glu	Thr	Glu	Val	Pro	Asp	Ala	
114				80						85					90	
115	Tyr	Asn	Met	Val	Pro	Pro	Lys	Val	Lys	Cys	Leu	Thr	Lys	Ile	Trp	
116				95						100					105	
117	His	Pro	Asn	Ile	Thr	Glu	Thr	Gly	Glu	Ile	Cys	Leu	Ser	Leu	Leu	
118				110						115					120	

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```

119 Arg Glu His Ser Ile Asp Gly Thr Gly Trp Ala Pro Thr Arg Thr
120                               125          130          135
121 Leu Lys Asp Val Val Trp Gly Leu Asn Ser Leu Phe Thr Asp Leu
122                               140          145          150
123 Leu Asn Phe Asp Asp Pro Leu Asn Ile Glu Ala Ala Glu His His
124                               155          160          165
125 Leu Arg Asp Lys Glu Asp Phe Arg Asn Lys Val Asp Asp Tyr Ile
126                               170          175          180
127 Lys Arg Tyr Ala Arg
128                               185
131 (2) INFORMATION FOR SEQ ID NO: 3:
133   (i) SEQUENCE CHARACTERISTICS:
134       (A) LENGTH: 59 amino acids
135       (B) TYPE: amino acid
136       (C) STRANDEDNESS: single
137       (D) TOPOLOGY: linear
139   (vii) IMMEDIATE SOURCE:
140       (A) LIBRARY: U937NOT01
141       (B) CLONE: 1847
143   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :
145 Met Gly Lys Val Asn Val Ala Lys Leu Arg Tyr Met Ser Arg Asp
146                               5          10          15
147 Asp Phe Arg Val Leu Thr Ala Val Glu Met Gly Met Lys Asn His
148                               20          25          30
149 Glu Ile Val Pro Gly Ser Leu Ile Ala Ser Ile Ala Ser Leu Lys
150                               35          40          45
151 His Gly Gly Cys Asn Lys Val Leu Arg Glu Leu Val Lys His
152                               50          55
155 (2) INFORMATION FOR SEQ ID NO: 4:
157   (i) SEQUENCE CHARACTERISTICS:
158       (A) LENGTH: 338 amino acids
159       (B) TYPE: amino acid
160       (C) STRANDEDNESS: single
161       (D) TOPOLOGY: linear
164   (vii) IMMEDIATE SOURCE:
165       (A) LIBRARY: HMC1NOT01
166       (B) CLONE: 9337
168   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
170 Met Leu Glu Thr Phe Gly His Leu Val Ser Val Gly Trp Glu Thr
171                               5          10          15
172 Thr Leu Glu Asn Lys Glu Leu Ala Pro Asn Ser Asp Ile Pro Glu
173                               20          25          30
174 Glu Glu Pro Ala Pro Ser Leu Lys Val Gln Glu Ser Ser Arg Asp
175                               35          40          45
176 Cys Ala Leu Ser Ser Thr Leu Glu Asp Thr Leu Gln Gly Gly Val
177                               50          55          60
178 Gln Glu Val Gln Asp Thr Val Leu Lys Gln Met Glu Ser Ala Gln
179                               65          70          75
180 Glu Lys Asp Leu Pro Gln Lys Lys His Phe Asp Asn Arg Glu Ser

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181		80		85		90
182	Gln Ala Asn Ser Gly Ala Leu Asp Thr Asn Gln Val Ser Leu Gln					
183		95		100		105
184	Lys Ile Asp Asn Pro Glu Ser Gln Ala Asn Ser Gly Ala Leu Asp					
185		110		115		120
186	Thr Asn Gln Val Leu Leu His Lys Ile Pro Pro Arg Lys Arg Leu					
187		125		130		135
188	Arg Lys Arg Asp Ser Gln Val Lys Ser Met Lys His Asn Ser Arg					
189		140		145		150
190	Val Lys Ile His Gln Lys Ser Cys Glu Arg Gln Lys Ala Lys Glu					
191		155		160		165
192	Gly Asn Gly Cys Arg Lys Thr Phe Ser Arg Ser Thr Lys Gln Ile					
193		170		175		180
194	Thr Phe Ile Arg Ile His Lys Gly Ser Gln Val Cys Arg Cys Ser					
195		185		190		195
196	Glu Cys Gly Lys Ile Phe Arg Asn Pro Arg Tyr Phe Ser Val His					
197		200		205		210
198	Lys Lys Ile His Thr Gly Glu Arg Pro Tyr Val Cys Gln Asp Cys					
199		215		220		225
200	Gly Lys Gly Phe Val Gln Ser Ser Ser Leu Thr Gln His Gln Arg					
201		230		235		240
202	Val His Ser Gly Glu Arg Pro Phe Glu Cys Gln Glu Cys Gly Arg					
203		245		250		255
204	Thr Phe Asn Asp Arg Ser Ala Ile Ser Gln His Leu Arg Thr His					
205		260		265		270
206	Thr Gly Ala Lys Pro Tyr Lys Cys Gln Asp Cys Gly Lys Ala Phe					
207		275		280		285
208	Arg Gln Ser Ser His Leu Ile Arg His Gln Arg Thr His Thr Gly					
209		290		295		300
210	Glu Arg Pro Tyr Ala Cys Asn Lys Cys Gly Lys Ala Phe Thr Gln					
211		305		310		315
212	Ser Ser His Leu Ile Gly His Gln Arg Thr His Asn Arg Thr Lys					
213		320		325		330
214	Arg Lys Lys Lys Gln Pro Thr Ser					
215		335				
218	(2) INFORMATION FOR SEQ ID NO: 5:					
220	(i) SEQUENCE CHARACTERISTICS:					
221	(A) LENGTH: 456 amino acids					
222	(B) TYPE: amino acid					
223	(C) STRANDEDNESS: single					
224	(D) TOPOLOGY: linear					
226	(vii) IMMEDIATE SOURCE:					
227	(A) LIBRARY: HMC1NOT01					
228	(B) CLONE: 9476					
230	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :					
232	Met Lys Ile Glu Glu Val Lys Ser Thr Thr Lys Thr Gln Arg Ile					
233		5		10		15
234	Ala Ser His Ser His Val Lys Gly Leu Gly Leu Asp Glu Ser Gly					
235		20		25		30

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```

236 Leu Ala Lys Gln Ala Ala Ser Gly Leu Val Gly Gln Glu Asn Ala
237                               35                      40                      45
238 Arg Glu Ala Cys Gly Val Ile Val Glu Leu Ile Glu Ser Lys Lys
239                               50                      55                      60
240 Met Ala Gly Arg Ala Val Leu Leu Ala Gly Pro Pro Gly Thr Gly
241                               65                      70                      75
242 Lys Thr Ala Leu Ala Leu Ala Ile Ala Gln Glu Leu Gly Ser Lys
243                               80                      85                      90
244 Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser Thr Glu
245                               95                     100                     105
246 Ile Lys Lys Thr Glu Val Leu Met Glu Asn Phe Arg Arg Ala Ile
247                               110                     115                     120
248 Gly Leu Arg Ile Lys Glu Thr Lys Glu Val Tyr Glu Gly Glu Val
249                               125                     130                     135
250 Thr Glu Leu Thr Pro Cys Glu Thr Glu Asn Pro Met Gly Gly Tyr
251                               140                     145                     150
252 Gly Lys Thr Ile Ser His Val Ile Ile Gly Leu Lys Thr Ala Lys
253                               155                     160                     165
254 Gly Thr Lys Gln Leu Lys Leu Asp Pro Ser Ile Phe Glu Ser Leu
255                               170                     175                     180
256 Gln Lys Glu Arg Val Glu Ala Gly Asp Val Ile Tyr Ile Glu Ala
257                               185                     190                     195
258 Asn Ser Gly Ala Val Lys Arg Gln Gly Arg Cys Asp Thr Tyr Ala
259                               200                     205                     210
260 Thr Glu Phe Asp Leu Glu Ala Glu Glu Tyr Val Pro Leu Pro Lys
261                               215                     220                     225
262 Gly Asp Val His Lys Lys Lys Glu Ile Ile Gln Asp Val Thr Leu
263                               230                     235                     240
264 His Asp Leu Asp Val Ala Asn Ala Arg Pro Gln Gly Gly Gln Asp
265                               245                     250                     255
266 Ile Leu Ser Met Met Gly Gln Leu Met Lys Pro Lys Lys Thr Glu
267                               260                     265                     270
268 Ile Thr Asp Lys Leu Arg Gly Glu Ile Asn Lys Val Val Asn Lys
269                               275                     280                     285
270 Tyr Ile Asp Gln Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe
271                               290                     295                     300
272 Val Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Thr Tyr Leu
273                               305                     310                     315
275 His Arg Ala Leu Glu Ser Ser Ile Ala Pro Ile Val Ile Phe Ala
276                               320                     325                     330
277 Ser Asn Arg Gly Asn Cys Val Ile Arg Gly Thr Glu Asp Ile Thr
278                               335                     340                     345
279 Ser Pro His Gly Ile Pro Leu Asp Leu Leu Asp Arg Val Met Ile
280                               350                     355                     360
281 Ile Arg Thr Met Leu Tyr Thr Pro Gln Glu Met Lys Gln Ile Ile
282                               365                     370                     375
283 Lys Ile Arg Ala Gln Thr Glu Gly Ile Asn Ile Ser Glu Glu Ala
284                               380                     385                     390
285 Leu Asn His Leu Gly Glu Ile Gly Thr Lys Thr Thr Leu Arg Tyr

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## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09840787.txt

Output Set: N:\CRF3\06152001\I840787.raw

L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:1081 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1085 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24